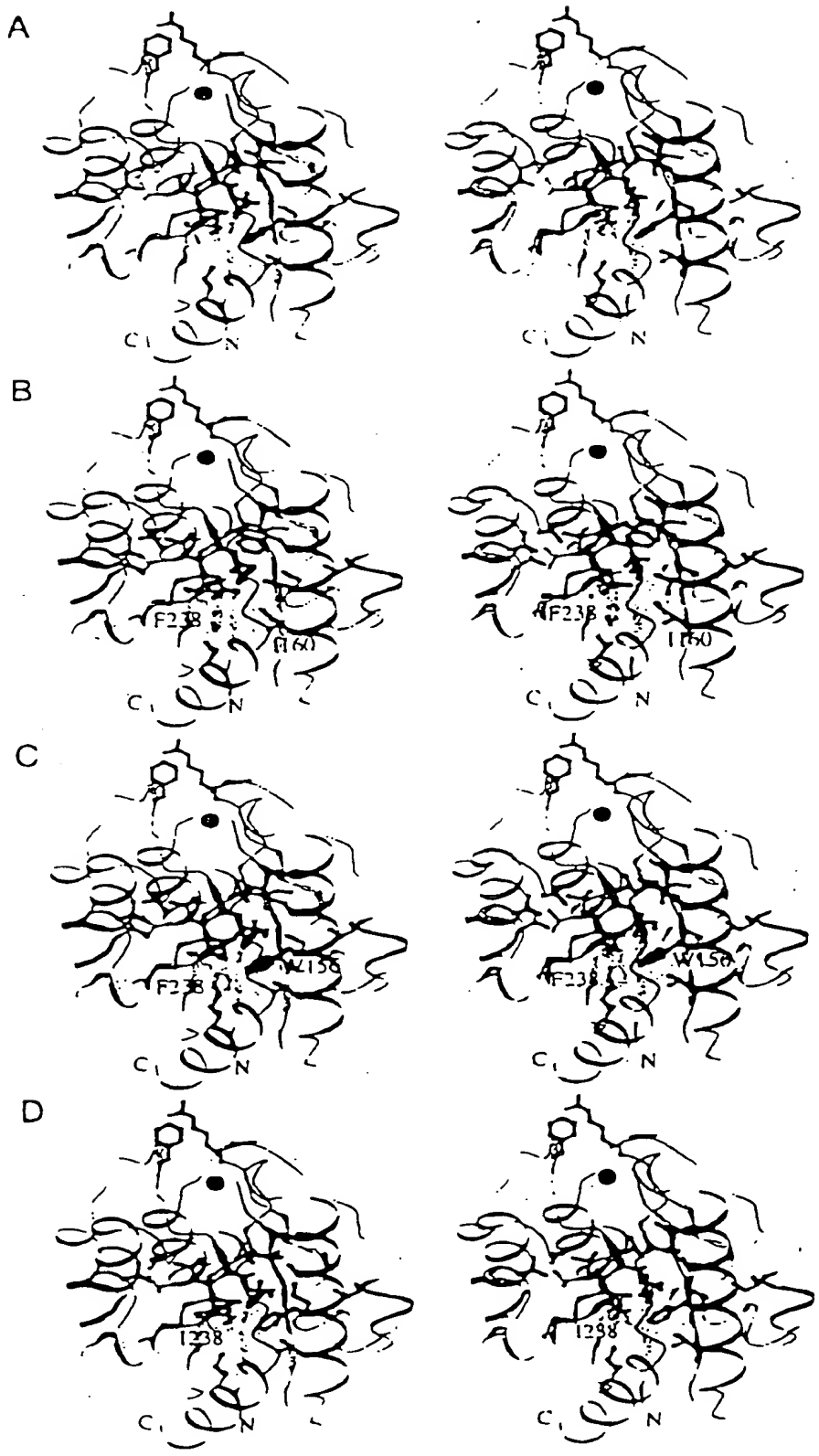

Fig. 1

Fig 1 E - Cont

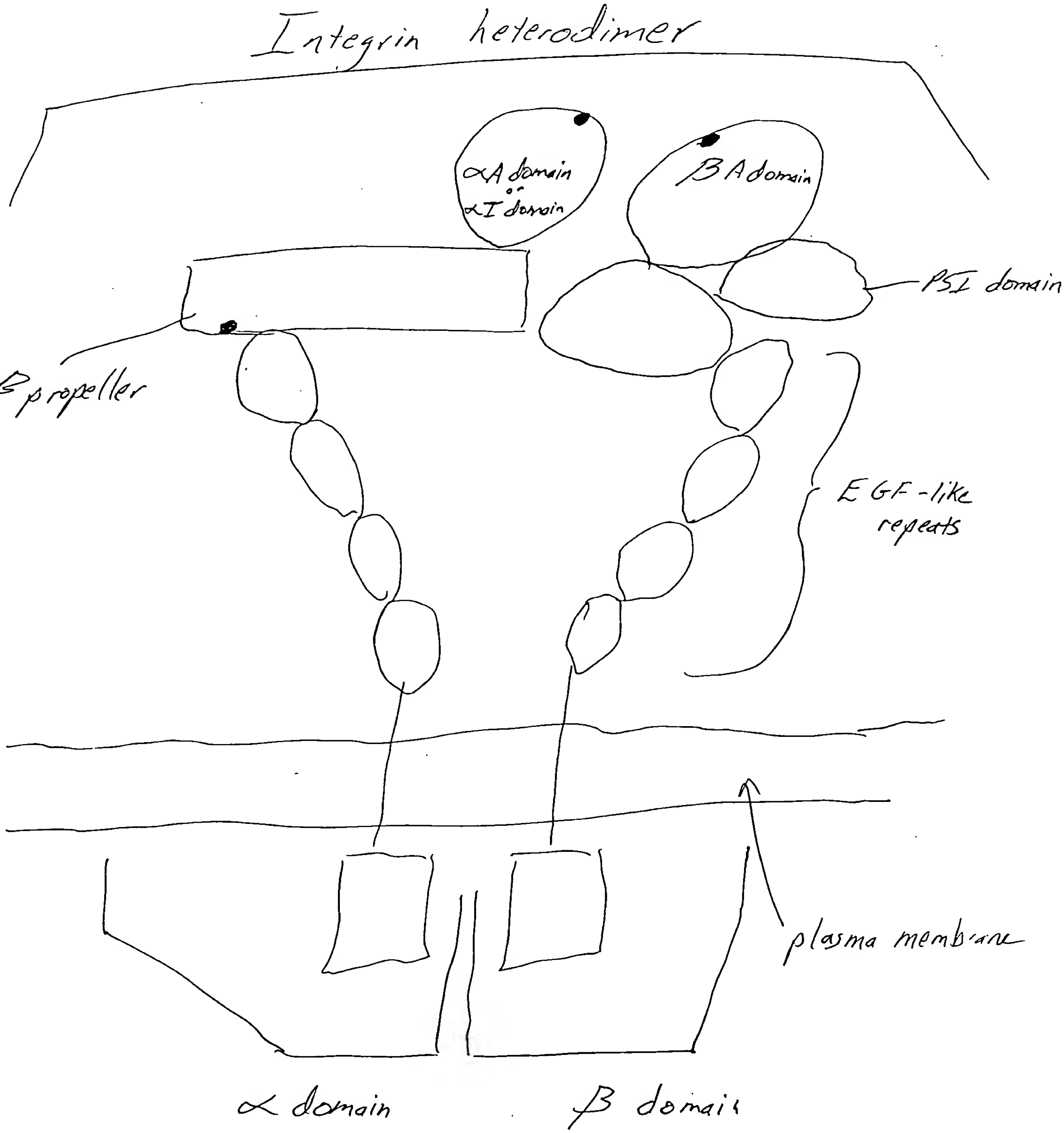
Integrin heterodimer
αA domain
or
αI domain
β A domain
PSI domain
β propeller
EGF-like
repeats
plasma membrane
α domain
β domain

Fig 1F

Sequence
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TQLLGRTHTATGIRKVVRELFNITNGARKNAFKILVVITDGEKFGDPLGYEDVIPEAD

REGVIRYVIGVGDAFRSEKSRQELNTIASKPPRDHVFQVNNFEALKTIQNQLREKIFA

IEGTQTGSSSSFEHEMSQEGFSAAITSNGPLLSTVGSYDWAGGVFLYTSKEKSTFINM

TRVDSDMNDAYLGYAAAIILRNRVQSLVLGAPRYQHIGLVAMFRQNTGMWESNANVKG

TQIGAYFGASLCSVDVDSNGSTDLVLIGAPHYYEQTRGGQVSVCPLPRGQRARWQCDA

VLYGEQGQPWGRFGAALTVLGDVNGDKLTDVAIGAPGEEDNRGAVYLFHGTSGSGISP

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SGRPHSRAVFNETKNSTRRQTQVLGLTQTCETLKLQLPNCIEDPVSPIVLRLNFSLVG

TPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGNDNICQDDLSITFSFMSLDCLVVGGP

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LVPVRLNQTVIWDRPQVTFSENLSSTCHTKERLPSHSDFLAELRKAPVVNCSIAVCQR

IQCDIPFFGIQEEFNATLKGNLSFDWYIKTSHNHLLIVSTAEILFNDSVFTLLPGQGA

FVRSQTETKVEPFEVPNPLPLIVGSSVGGLLLLALITAALYKLGFFKRQYKDMMSEGG
PPGAEPQ"

Fig 1F

```
BASE COUNT     1095 a   1271 c   1289 g   1085 t
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       61 ctccttccag ccatggctct cagagtcctt ctgttaacag ccttgacctt atgtcatggg
      121 ttcaacttgg acactgaaaa cgcaatgacc ttccaagaga acgcaagggg cttcgggcag
      181 agcgtggtcc agcttcaggg atccagggtg gtggttggag ccccccagga gatagtggct
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      301 cgcctgcagg tccccgtgga ggccgtgaac atgtccctgg gcctgtccct ggcagccacc
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      421 acgtatgtga aagggctctg cttcctgttt ggatccaacc tacggcagca gccccagaag
      481 ttcccagagg ccctccgagg gtgtcctcaa gaggatagtg acattgcctt cttgattgat
      541 ggctctggta gcatcatccc acatgacttt cggcggatga aggagtttgt ctcaactgtg
      601 atggagcaat taaaaaagtc caaaaccttg ttctctttga tgcagtactc tgaagaattc
      661 cggattcact ttaccttcaa agagttccag aacaacccta acccaagatc actggtgaag
      721 ccaataacgc agctgcttgg gcggacacac acggccacgg gcatccgcaa agtggtacga
      781 gagctgttta acatcaccaa cggagcccga aagaatgcct ttaagatcct agttgtcatc
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      901 agagagggag tcattcgcta cgtcattggg gtgggagatg ccttccgcag tgagaaatcc
      961 cgccaagagc ttaataccat cgcatccaag ccgcctcgtg atcacgtgtt ccaggtgaat
     1021 aactttgagg ctctgaagac cattcagaac cagcttcggg agaagatctt tgcgatcgag
     1081 ggtactcaga caggaagtag cagctccttt gagcatgaga tgtctcagga aggcttcagc
     1141 gctgccatca cctctaatgg ccccttgctg agcactgtgg ggagctatga ctgggctggt
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     1261 tcagacatga atgatgctta cttgggttat gctgccgcca tcatcttacg gaaccgggtg
     1321 caaagcctgg ttctgggggc acctcgatat cagcacatcg gcctggtagc gatgttcagg
     1381 cagaacactg gcatgtggga gtccaacgct aatgtcaagg gcacccagat cggcgcctac
     1441 ttcggggcct ccctctgctc cgtggacgtg gacagcaacg gcagcaccga cctggtcctc
     1501 atcggggccc cccattacta cgagcagacc cgagggggcc aggtgtccgt gtgccccttg
     1561 cccagggggc agagggctcg gtggcagtgt gatgctgttc tctacgggga gcagggccaa
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     1681 acggacgtgg ccattggggc cccaggagag gaggacaacc ggggtgctgt ttacctgttt
     1741 cacggaacct caggatctgg catcagcccc tcccatagcc agcggatagc aggctccaag
     1801 ctctctccca ggctccagta ttttggtcag tcactgagtg ggggccagga cctcacaatg
     1861 gatggactgg tagacctgac tgtaggagcc caggggcacg tgctgctgct caggtcccag
     1921 ccagtactga gagtcaaggc aatcatggag ttcaatccca gggaagtggc aaggaatgta
     1981 tttgagtgta atgatcaggt ggtgaaaggc aaggaagccg gagaggtcag agtctgcctc
     2041 catgtccaga agagcacacg ggatcggcta agagaaggac agatccagag tgttgtgact
     2101 tatgacctgg ctctggactc cggccgccca cattcccgcg ccgtcttcaa tgagacaaag
     2161 aacagcacac gcagacagac acaggtcttg gggctgaccc agacttgtga gaccctgaaa
     2221 ctacagttgc cgaattgcat cgaggaccca gtgagcccca ttgtgctgcg cctgaacttc
     2281 tctctggtgg gaacgccatt gtctgctttc gggaacctcc ggccagtgct ggcggaggat
     2341 gctcagagac tcttcacagc cttgtttccc tttgagaaga attgtggcaa tgacaacatc
     2401 tgccaggatg acctcagcat caccttcagt ttcatgagcc tggactgcct cgtggtgggt
     2461 gggccccggg agttcaacgt gacagtgact gtgagaaatg atggtgagga ctcctacagg
     2521 acacaggtca ccttcttctt cccgcttgac ctgtcctacc ggaaggtgtc cacactccag
     2581 aaccagcgct cacagcgatc ctggcgcctg gcctgtgagt ctgcctcctc caccgaagtg
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     2701 gaggtcacct ttaatatcac gtttgatgta gactctaagg cttcccttgg aaacaaactg
     2761 ctcctcaagg ccaatgtgac cagtgagaac aacatgccca gaaccaacaa aaccgaattc
     2821 caactggagc tgccggtgaa atatgctgtc tacatggtgg tcaccagcca tggggtctcc
     2881 actaaatatc tcaacttcac ggcctcagag aataccagtc gggtcatgca gcatcaatat
     2941 caggtcagca acctggggca gaggagcctc cccatcagcc tggtgttctt ggtgcccgtc
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     3061 agtacgtgcc acaccaagga gcgcttgccc tctcactccg actttctggc tgagcttcgg
     3121 aaggcccccg tggtgaactg ctccatcgct gtctgccaga gaatccagtg tgacatcccg
     3181 ttctttggca tccaggaaga attcaatgct accctcaaag gcaacctctc gtttgactgg
     3241 tacatcaaga cctcgcataa ccacctcctg atcgtgagca cagctgagat cttgtttaac
     3301 gattccgtgt tcaccctgct gccgggacag gggcgtttg tgaggtccca gacggagacc
     3361 aaagtggagc cgttcgaggt ccccaacccc ctgccgctca tcgtgggcag ctctgtcggg
     3421 ggactgctgc tcctggccct catcaccgcc gcgctgtaca agctcggctt cttcaagcgg
     3481 caatacaagg acatgatgag tgaagggggt cccccggggg ccgaacccca gtagcggctc
```

Fig 1.F

```
3541 cttcccgaca gagctgcctc tcggtggcca gcaggactct gcccagacca cacgtagccc
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3661 tttgtgtgtg tgcaagtgtg tatgtgcgtg tgtgcgagtg tgtgcaagtg tctgtgtgca
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3901 tctctggcgt gtgggtaggt gacggcagcg tagcctctcc ggcagaaggg aactgcctgg
3961 gctcccttgt gcgtgggtaa gccgctgctg ggttttcctc cgggagaggg gacggtcaat
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4081 cccgtcgcct gcgagcctgc ggcctgctgg agcctgcgca gcttggatgg atactccatg
4141 agaaaagccg tgggtggaac caggagcctc ctccacacca gcgctgatgc ccaataaaga
4201 tgcccactga ggaatcatga agcttccttt ctggattcat ttattatttc aatgtgactt
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4621 atttaaccag tcttcttttg atatactatt ttcatctctt gttattgcat ctgctgagtt
4681 aataaatcaa atatatgtca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa
//
```

Fig 2

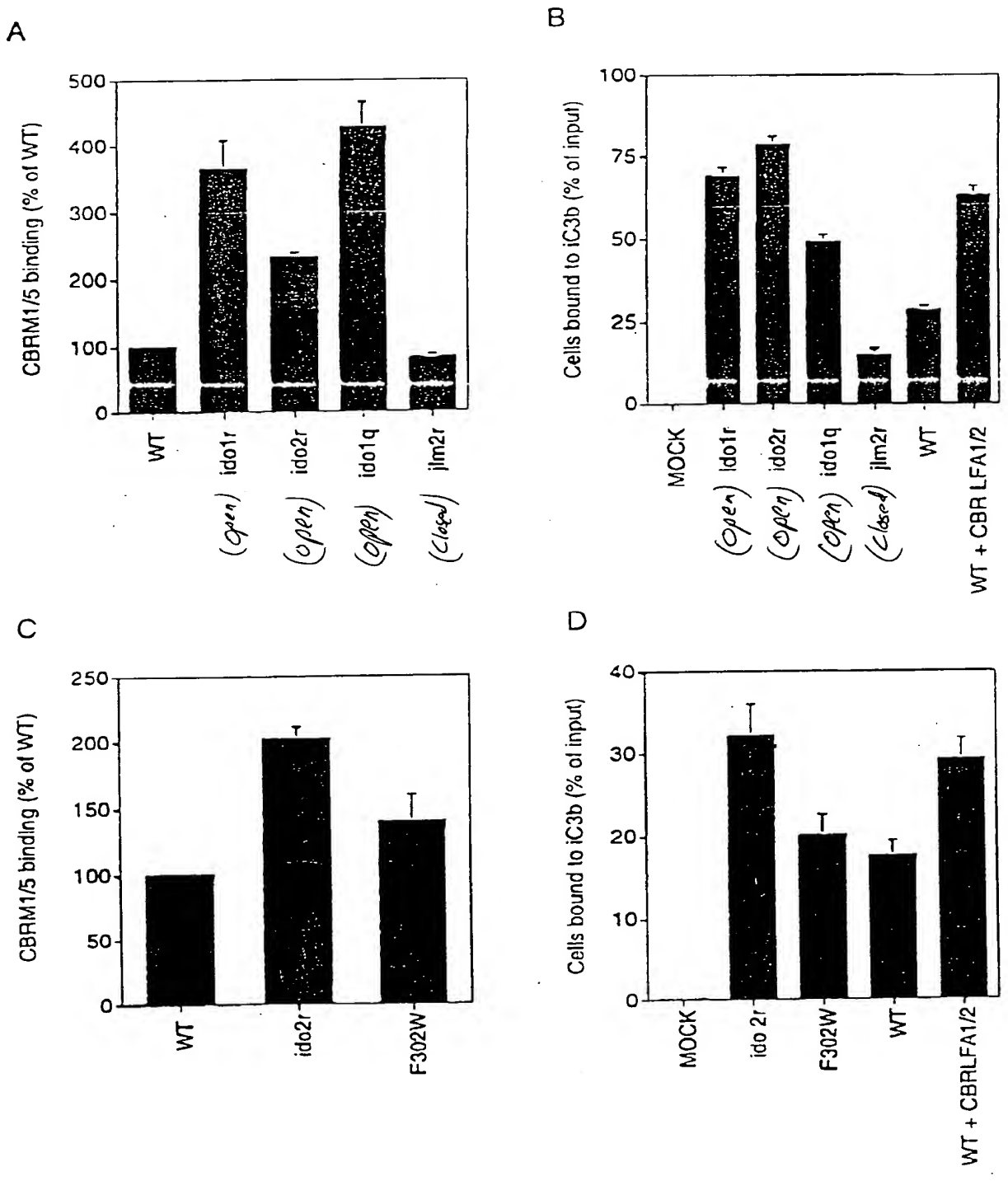

A
CBRM1/5 binding (% of WT)
500
400
300
200
100
0
WT
ido1r (open)
ido2r (open)
ido1q (open)
jlm2r (closed)
B
Cells bound to iC3b (% of input)
100
75
50
25
0
MOCK
ido1r (open)
ido2r (open)
ido1q (open)
jlm2r (closed)
WT
WT + CBR LFA1/2
C
CBRM1/5 binding (% of WT)
250
200
150
100
50
0
WT
ido2r
F302W
D
Cells bound to iC3b (% of input)
40
30
20
10
0
MOCK
ido 2r
F302W
WT
WT + CBRLFA1/2

Fig. 3

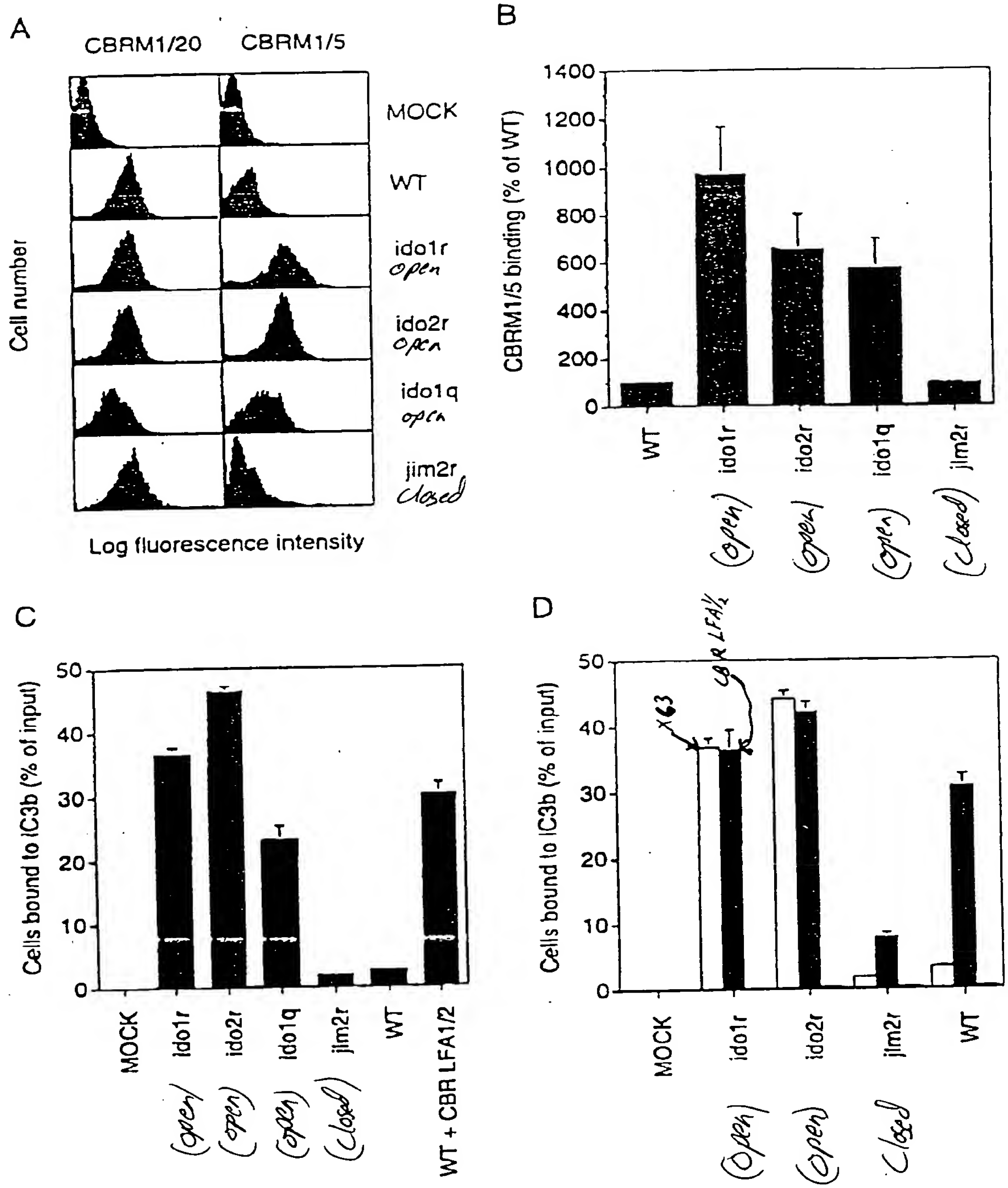
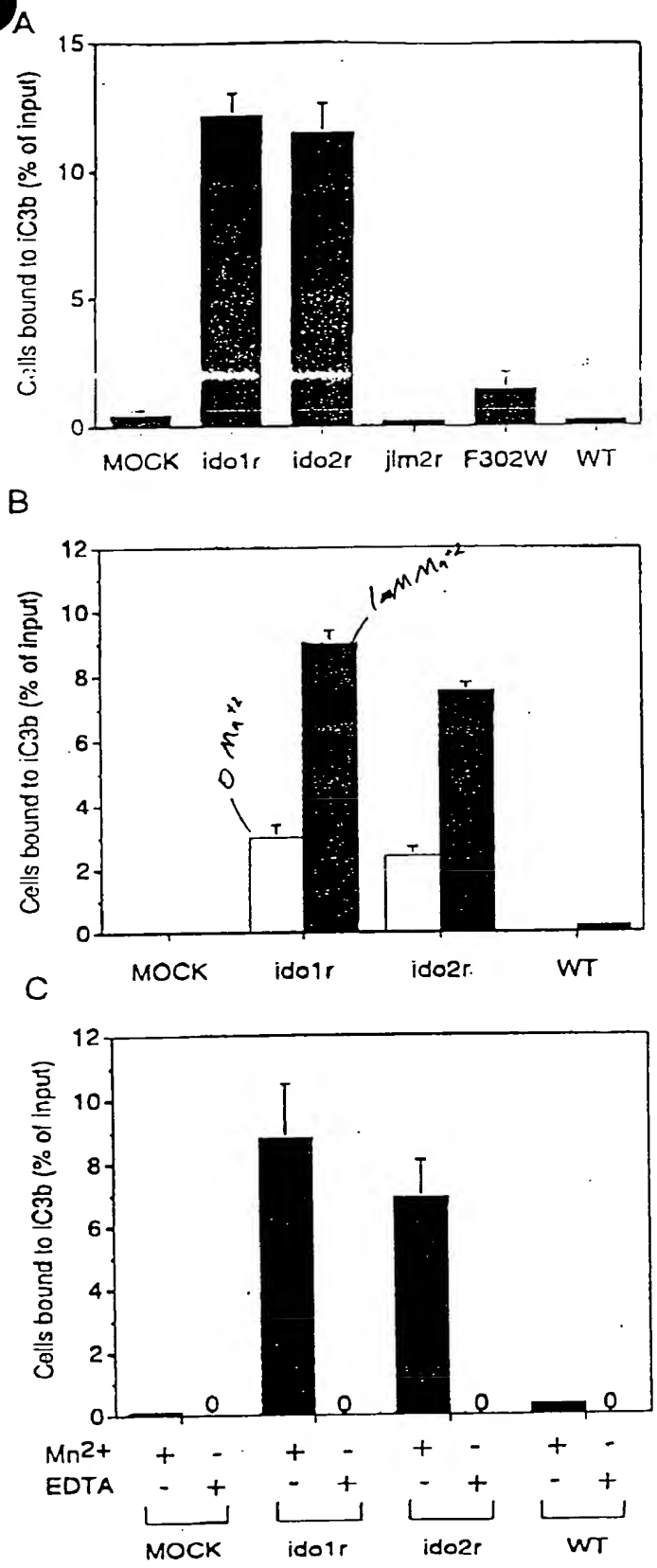

A
CBRM1/20
CBRM1/5
MOCK
WT
ido1r
open
ido2r
open
ido1q
open
jim2r
closed
Cell number
Log fluorescence intensity
B
CBRM1/5 binding (% of WT)
1400
1200
1000
800
600
400
200
0
WT
ido1r
ido2r
ido1q
jim2r
(open)
(open)
(open)
(closed)
C
Cells bound to IC3b (% of input)
50
40
30
20
10
0
MOCK
ido1r
ido2r
ido1q
jim2r
WT
WT + CBR LFA1/2
(open)
(open)
(open)
(closed)
D
Cells bound to IC3b (% of input)
50
40
30
20
10
0
CBR LFA1/2
MOCK
ido1r
ido2r
jim2r
WT
(Open)
(open)
closed

Fig 4


A
Cells bound to iC3b (% of input)
15
10
5
0
MOCK
ido1r
ido2r
jlm2r
F302W
WT
B
Cells bound to iC3b (% of input)
12
10
8
6
4
2
0
0 Mn++
1mM Mn++
MOCK
ido1r
ido2r
WT
C
Cells bound to iC3b (% of Input)
12
10
8
6
4
2
0
0
0
0
0
Mn2+ + - + - + - + -
EDTA - + - + - + - +
MOCK
ido1r
ido2r
WT

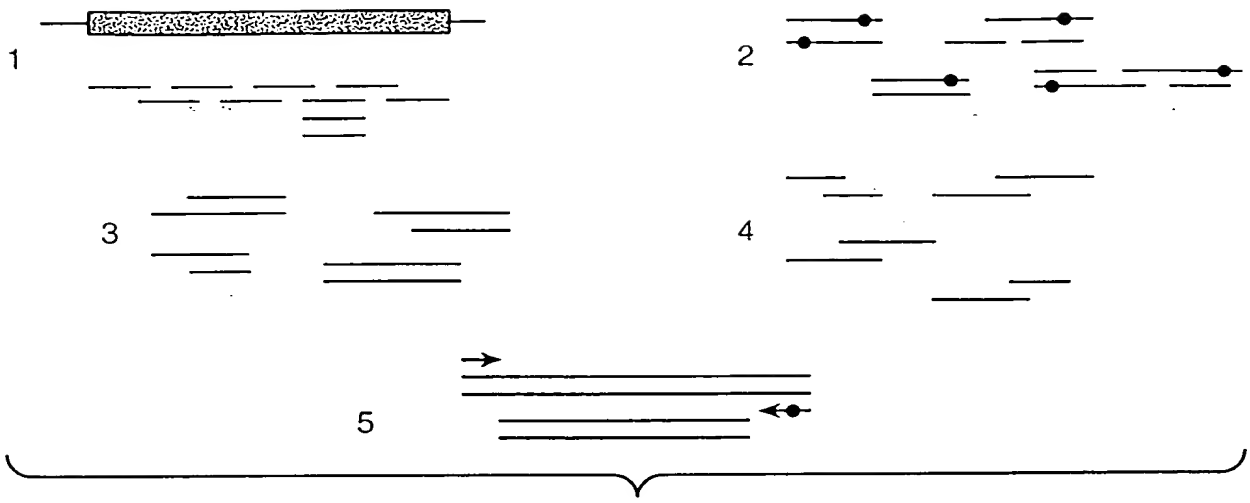

1
2
3
4
5

Fig 5

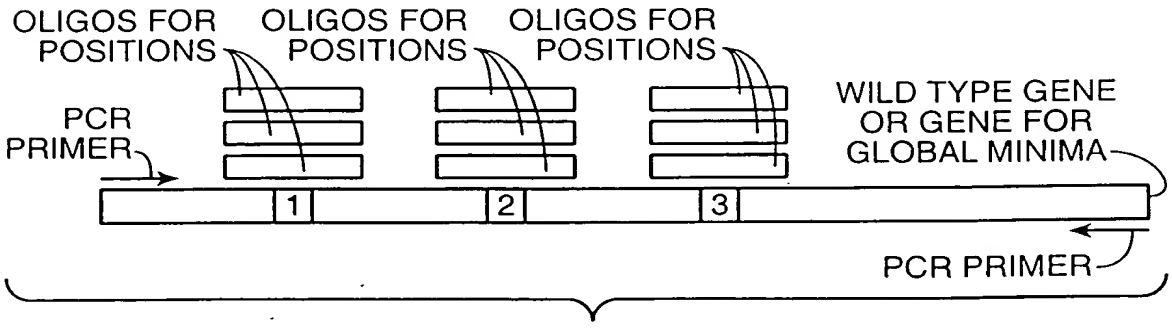
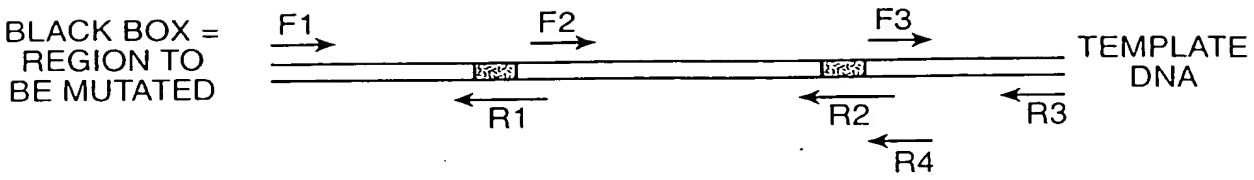

OLIGOS FOR POSITIONS
OLIGOS FOR POSITIONS
OLIGOS FOR POSITIONS
PCR PRIMER
WILD TYPE GENE OR GENE FOR GLOBAL MINIMA
1
2
3
PCR PRIMER

Fig 6



STEP 1: SET UP 3 PCR REACTIONS:

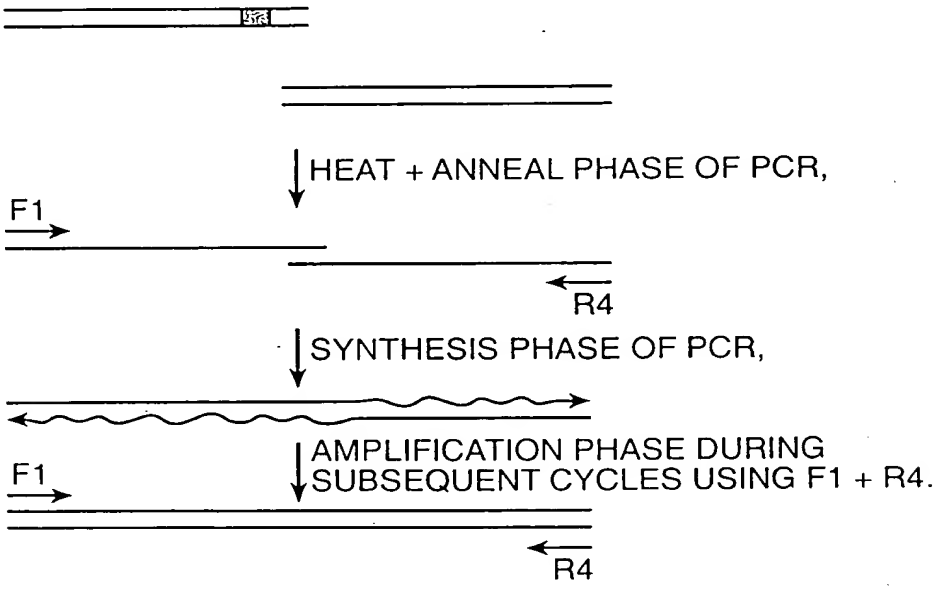
PRODUCTS:

TUBE 1:

TUBE 2:

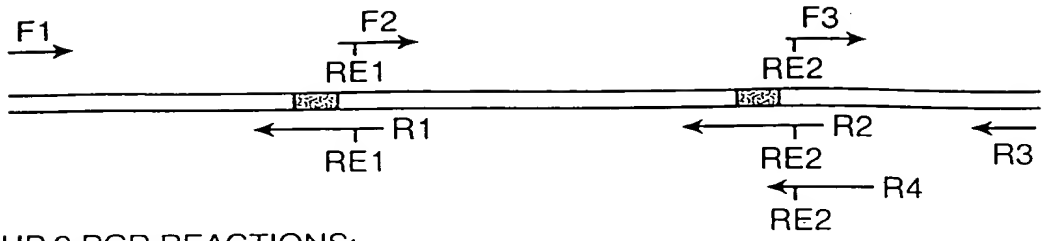
TUBE 3:

STEP 2: SET UP PCR REACTION WITH PRODUCTS OF TUBE 1 + PRODUCTS TUBE 2 + F1 + R4.



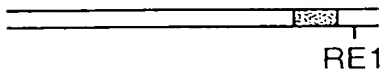
STEP 3: REPEAT STEP 2 USING PRODUCT FROM STEP 2 + PRODUCT FROM STEP 1, TUBE 3 + PRIMERS F1 + R3.

FIG. 7

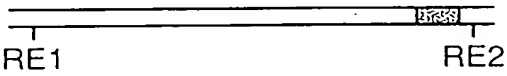


STEP 1: SET UP 3 PCR REACTIONS:

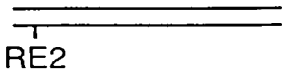
TUBE 1:



TUBE 2:

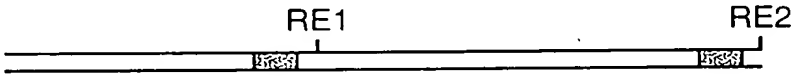


TUBE 3:

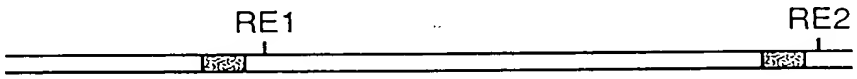


STEP 2: DIGEST PRODUCTS FROM STEP 1 WITH SUITABLE RESTRICTION ENDONUCLEASES.

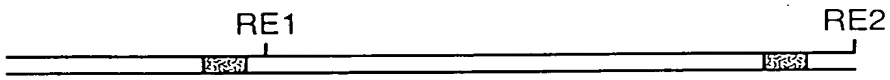
STEP 3: LIGATE DIGESTED PRODUCT FROM STEP 2, TUBE 2 WITH DIGESTED PRODUCT FROM STEP 2, TUBE 1.



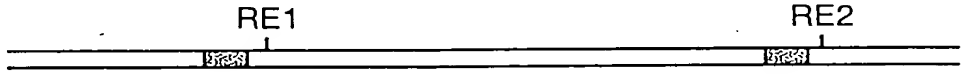
STEP 4: AMPLIFY VIA PCR LIGATED PRODUCTS OF STEP 3 WITH F1 + R4.



STEP 5: DIGEST AMPLIFIED PRODUCT OF STEP 4 WITH RESTRICTION ENDONUCLEASE #2.



STEP 6: LIGATE PRODUCT FROM STEP 5 WITH PRODUCT FROM STEP 2, TUBE 3.



STEP 7: AMPLIFY PRODUCT FROM STEP 6 WITH F1 + R3.

Fig 8

DIAGRAM 3

Fig. 9